

Dorset and Thule Divergence From East Central Asian Roots

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ABSTRACT The history of the immigration of East Asians to America during the last glacial period remains controversial. In an attempt to add critical data to this problem, a large sample of whole teeth derived from Southeast Asian, Mongolian, Thule, Western Inuit, and pre-Inca (Huari) people was quantified (N = 4,507 teeth from 495 individuals; ~30 variables per tooth). Multivariate analysis helped establish that all Native Americans were likely derived from one ancient, extinct population that resided in the region of Mongolia (east Central Asia), and that Mongolians and Southeast Asians are two independent groups. A controversial and enigmatic Central Canadian Arctic "Thule culture Inuit" group on Southampton Island that survived until 1902 was identified as a relic, mainly Paleoeskimo Dorset community. Surprisingly, there was little, or no, indication of Dorset-to-Thule gene flow. Cumulatively, the data suggest that a small population of Paleoindian founders remained resident in Beringia, may have blocked further immigration, and were the antecedents to the Thule/Inuit. With the confluence of the Arctic and Pacific oceans at the breakup of Beringia, the resulting increased availability of marine animal food sources allowed this population to increase in size and expand throughout the eastern Arctic. *Am J Phys Anthropol* 106:207-218, 1998. © 1998 Wiley-Liss, Inc.

The concept championed by Szathmáry (Szathmáry and Ossenberg, 1978; Szathmáry 1979, 1981, 1993, 1994, 1996), that one very early migratory wave into Beringia occurred during the Wisconsinan glaciation, has been strongly supported by the weight of genetic data (Bonatto and Salzano, 1997a,b; Forster et al., 1996; Karafet et al., 1997; Kolman et al., 1997; Merriwether et al., 1995, 1996). Nei (1995) further posited that at approximately 30,000 BP (before present) founder groups expanded concentrically out of the general region of present-day Mongolia. Both genetic (Merriwether et al., 1996) and odontometric data (Turner, 1984, 1989, 1994; Shields, 1996) suggest that one component of these pioneers diffused into Beringia. Linguistic (Greenberg, 1987), and some

anthropological divergence among Native Americans (Turner 1994, 1995), and archaeological findings (West, 1996), suggest that multiple more recent waves of migration across Beringia occurred over an extended time.

In an attempt to add relevant information for a formulation of a more definitive origin of Native Americans, we tested the following hypotheses: 1) the immediate ancestors of all Native Americans, including the Inuit, were derived from a single east Central

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TABLE 1. Percentage of each population sample that had bifid premolars

Ethnic group	Bifid P ¹	Non-bifid P ¹	%	Bifid P ²	Non-bifid P ²	%	Bifid P ₁	Non-bifid P ₁	%	Bifid P ₂	Non-bifid P ₂	%
Southeast Asian	0	32	—	0	48	—	2	63	3.08	0	61	—
Mongolian	0	93	—	0	101	—	0	77	—	0	84	—
Western Inuit	1	48	2.04	0	55	—	1	66	1.49	0	63	—
Thule	0	75	—	0	84	—	0	92	—	0	91	—
Dorset	0	16	—	0	21	—	0	34	—	0	31	—
Pre-Inca	1	19	5.00	0	22	—	12	43	21.82	0	55	—

Asian population, and 2) an isolated, and now extinct population from Southampton Island was a relic, mainly Dorset, (Paleoeskimo) population, and of the samples studied, the best representative of the ancient progenitors that first entered America. In our search for associations among Thule culture Inuit, Western Inuit (Eskimo), Peruvian Indians, and three East Asian populations, ~30 complete tooth measurement variables and four derived variables per tooth were used.

MATERIALS AND METHODS

In previous reports (Shields and Jones, 1996; Shields, 1996) the methods employed have been discussed, along with the non-Thule and non-Dorset samples utilized, a description of the global dental phenotype, its complex morphogenetics, and the biology of its microevolution. Briefly, periapical dental radiographs were taken on skulls held in museum collections (exceptions being some Southern Chinese and the total Vietnamese sample, which were taken on clinical patients). The X-rays were enlarged, and variables were digitized into a computer. The variables digitized are as follows: A) *areas*; tooth profile area (tarea), crown area (tcrown), root area (troot), the coronal and apical halves of the root, and root pulp profile area (parea). On a periapical X-ray the crown is very clearly identified both mesially and distally by the cemento-enamel junction (where the enamel meets the root), and its apical aspect is delineated by a line drawn between these two points. B) *Distances*; the enamel thickness was measured 1 mm from the dento-enamel junction (DEJ) (menamel = mesial and denamel = distal enamel depth), the distance between crown contact points (crown), width of the root at

the DEJ, and halfway along the root, the length of the tooth; and C) *derived shape variables*; the relative pulp area (pratio = pulp area/tooth area), crratio = crown area/root area, elongation = tooth width at the DEJ/tooth height, and root robustness, 1) root area (lower half of the root area/upper half), and 2) rootratio (root/DEJ). As discussed previously (Shields, 1996), an examination of the canonical discriminant analysis of males and females from each ethnic stock, by each tooth element, showed that the sexes from each stock, although clearly independent (sexually dimorphic), were closely associated. Both sexes were combined for all analyses.

Only the buccal root in Tomes' premolars and buccal roots in mandibular molars with three roots were measured. The prevalence of bifid premolars is shown in Table 1. The Pre-Inca were the only population to have a substantial number of bifid mandibular premolars. Human root morphologic variation and its biology will be a topic of a future publication.

The samples for the analysis consisted of the following: Southern Chinese 20 ♂/18 ♀ individuals (153 ♂/189 ♀ teeth); Vietnamese 11 ♂/11 ♀ (179/182); Mongolians 58 ♂/61 ♀ (528/529); Western Inuit (Kodiak Island) 21 ♂/31 ♀ (255/497); Thule 86 ♂/81 ♀ (644/515) of which 44 ♂/36 ♀ 252/177 were from northwest Greenland (coastal Hayes Peninsula) and the rest from Canada (Fig. 1); Southampton Island ("Dorset") 30 ♂/18 ♀ (218/99); and Pre-Inca (Huari Empire) 27 ♂/22 ♀ (310/209); total: 253 ♂/242 ♀ individuals (2,287 ♂/2,220 ♀ teeth).

Because of restrictions on the acceptance of a tooth for analysis (i.e., little wear, not severely rotated or tipped, not microdont, or with hypercementosis), along with the in-

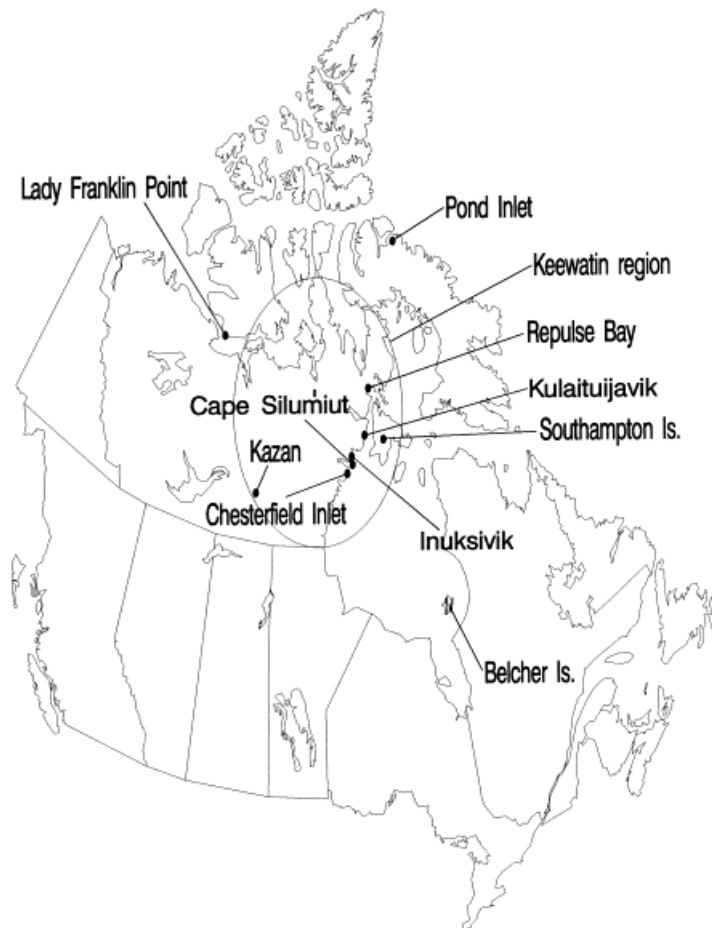


Fig. 1. Thule/"Dorset" skeletal materials used in this study were derived from central Canadian sites. Keewatin is a Northwest Territory district from which several unmarked sites exist.

creased prevalence of missing teeth in skeletal material, the presence of both antimeres was not frequent. For example, 27% (131/483) of Thule teeth used for the multivariate analysis were antimeres. Because all teeth within an individual are correlated, it is believed that the inclusion of antimeres did not add significant bias to the data and likely helped mitigate some measurement errors. This methodology has proven very powerful for the identification of minor, but biologically significant, human dental variation (Shields et al., 1990).

For most analyses all teeth were combined. For selected tests morphogenetic, functional, and size-similar tooth elements were used as follows: mandibular first and

second molars, mandibular third molars, maxillary central incisors, maxillary lateral incisors, maxillary canines, mandibular canines, maxillary premolars, mandibular premolars, mandibular central incisors, and mandibular lateral incisors. Only teeth with little wear (wear = 0, 1, or 2) were used in the multivariate analyses. Wear was a ranked variable that ranged from zero (no attrition) to six (attrition extending close to the dentino-enamel junction). Each tooth was assessed from the X-ray for the relative loss of crown structure in relation to the DEJ (no measurement was done). Moderate (wear = 3 or 4) and severe attrition are frequent findings that restrict the sample size for tooth crown area comparisons.

Mainly because of the programmed steady accretion of secondary dentin, pulp area steadily diminishes through time (Shields et al., 1990). For example in Mongolian males, the pulp area of first and second mandibular molars with wear less than 3 had a significant negative linear regression with age ($N = 63$, $\text{parea} = 23.12 - 0.27 * \text{age}$; $P = .001$). The distribution of pulp area values was not normally distributed (Shapiro-Wilk = .009), being skewed to the right on age (0.82) and mildly leptokurtic (0.26). A few older people with relatively mild wear for some teeth caused the drawing out of the distribution, but this mild contamination was roughly balanced around the mean of mild wear by pristine teeth from a few young individuals. Any potential error is diluted when root variables are added in the multivariate analysis, thus limiting one variable's inordinate effect on the total dental phenotype. The objective is comparability among populations. Pulp area also varies inversely with wear ($N = 73$; $\text{parea} = 18.22 - 1.98 * \text{wear}$; $P = .001$), because wear causes a third type of dentin formation (tertiary dentin). Of course wear and age are positively correlated. The distribution of wear values also fits the pattern seen in pulp area. For those crowns within the category considered as mild wear, a few crowns were unworn and a few had wear extending 2/7 of the crown, but the mean for each tooth group should approximate 1/7. Whereas crown and pulp areas are altered by use and age, root areas are mainly unaffected ($N = 63$, $\text{parea} = 84.24 + 0.08 * \text{age}$; $P = .78$).

Provenience is difficult to establish for much of the Arctic Paleoindian, Paleoarctic (Dixon, 1985), and Inuit material (Hrdlička, 1910; McCartney, 1977). One reason is the tendency for succeeding Paleoindian/Neoinuit cultures to build over, reuse, and salvage older dwellings from their predecessors (Park, 1993). Sites may span several generations and cultures. Some of the skeletal material from Southampton Island lacked precise provenience because it was collected by a whaling ship captain (Mathiassen, 1927a; Hrdlička, 1910).

RESULTS

Figure 2 shows the two-dimensional (2-D) graphical results of the canonical discriminant analysis of the global dental phenotype. A clear separation on Can1 can be seen between Southeast Asia samples, and the major cluster is composed of Mongolians and all Native Americans. Can1 represents 40% of the variance. Can2 separated the population major subcluster of Mongolia-Western Inuit-Southampton Island ("Dorset")-Pre-Inca from Thule and Southeast Asia, and represented 31% of the variance. Figure 3 gives a better three-dimensional view of the relationships among the populations and accounts for 88% of the variance (Wilks' Lambda = 0.60, $F_{(72,11812)} = 16.3$; $P < .0001$).

Several variables were more important in separating the populations (especially tooth height, elongation, and enamel depth, Table 2). The vectors express the power of each variable to discriminate. The length of the variable vectors seen in the 2-D plots (Figs. 2, 4) were mirrored in multiple means tests, by tooth element, among the populations. Individual tooth elements generally reflected the combined representations. The most discriminating variables were highly significant ($P < .0001$) for all, or most, tooth elements (data not presented). As opposed to the multivariate analyses, the univariate analyses were unencumbered by the necessity for each tooth to have all measurement variables. From these data, microevolution in tooth morphology among the ethnic stocks can be characterized. The pre-Inca and the Western Inuit had very thick enamel. The pre-Inca also tended to have relatively large roots. The Thule and Southampton Island "Dorset" teeth were rotund with relative large pulp areas, whereas the trend in Mongolian teeth was to be more gracile. The southern Chinese and Vietnamese had long teeth with large crowns, and the Thule had short teeth.

Table 3 gives the squared distances between the population samples. An examination of the three-dimensional dispersion of the centroids among the global dental phenotypes in Figure 3 shows three general types of population clusters: 1) *tight*—Southamp-

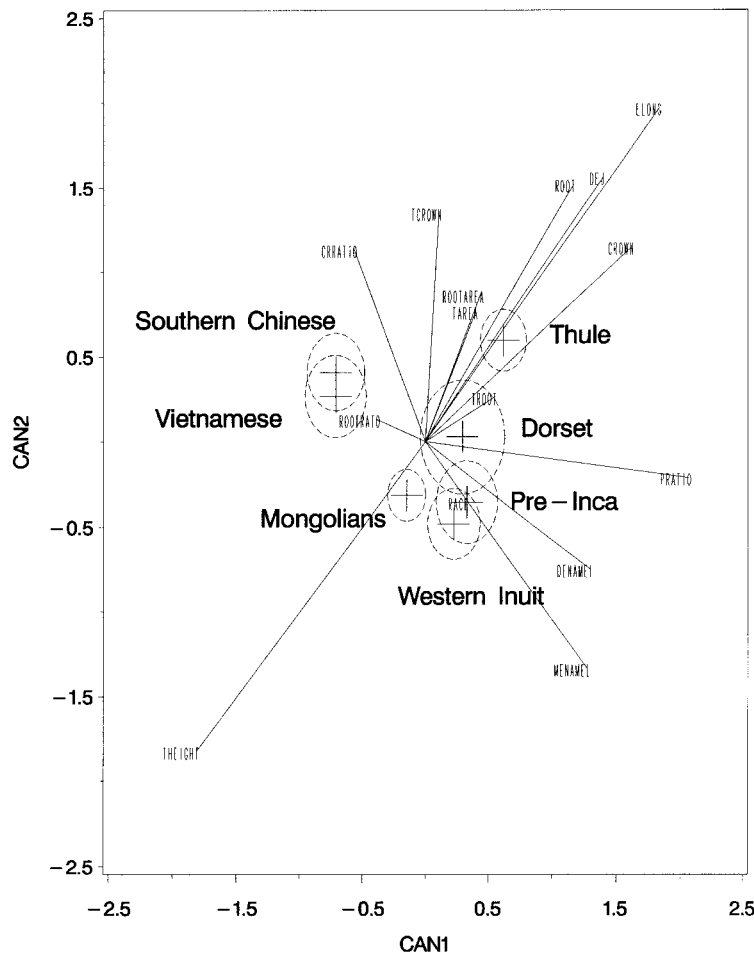


Fig. 2. A two-dimensional (2-D) comparison among the ethnic stocks (marked "race") of all tooth elements and both sexes combined. Canonical discriminant analysis explaining 71% of the variation, with 99% confidence regions drawn from the mean of each ethnic stock (cross signifies centroid). Vectors are drawn representing the contribution (structural coefficients) of each variable in

the separation to both canonical dimensions. Frequently the variables near the epicenter of the standardized canonical coefficient "starburst" are not significant. Because of the great number of observations ($n = 2,188$), individual data points are not shown, as they obscure the central tendencies.

ton Island "Dorset"/Western Inuit/Pre-Inca Native Americans form a tight cluster with Mongolia. The Thule closely associates with Southampton Island and appears as a direct extension away from Southampton Island's position on this cluster. Southampton Island is clearly an independent population from Thule. The two Southeast Asian populations closely associate as a pair; 2) *intermediate*—Mongolia is positioned midway between Southeast Asians and Thule/Pre-Inca. South-

ampton Island and Western Inuit are loosely associated with one or the other Southeast Asian population; and 3) *loose*—Southeast Asia and Native Americans (especially Thule and Pre-Inca) associate relatively uniformly at long ranges.

During the examination of the periapical X-rays, it became apparent that a unique trait was prevalent within Thule and Southampton Island populations. The trait was characterized as an abbreviated, or short,

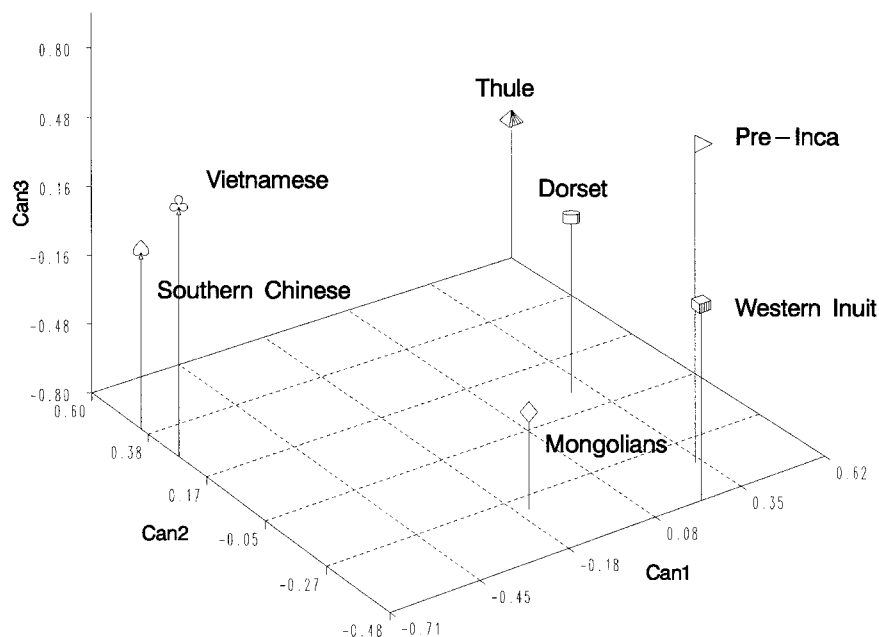


Fig. 3. The global dental phenotype, which for each ethnic stock is a composite of all dental variables and both sexes, is plotted in 3-D. All three significant canonical variables account for 88% of the variance. Each ethnic stock is depicted by a centroid as marked with a symbol.

root and we felt that it was observed preferentially in all second premolars and maxillary canines. The sex ratio of the trait among all teeth was approximately equal (46/55). After digitization, an examination of the distribution of tooth area, root area, and tooth height found that these variables were all normally distributed (Shapiro-Wilk statistic), with no signs of a dichotomy. Regression coefficients of root area on age were not significantly different from zero. Thus, root size variant was not a "trait" itself, but merely the most extreme manifestation of the continuous distribution of the generalized rotund nature of tooth structure in Thule/Southampton Island.¹

DISCUSSION

Associations of the global dental phenotype among the population samples clearly showed a conspicuous empty space near the origin of Figure 2. An unmeasured, extinct

antecedent east Central Asian population likely resides in this space. This ancestral east Central Asian population is the probable source, or Asian root, from which both Mongolians and Native Americans were derived. The potential east Central Asian origins of all Native Americans is compatible with genetic (Bonatto and Salzano, 1997a,b; Merriwether et al., 1996; Neel et al., 1994) and other dental data (Turner 1984, 1989). Mongolia's position at the apex of a near isosceles triangle with Thule and Pre-Inca at its base, further suggests common ancient ancestry (Thule being the furthest). A second but larger triangle also exists encompassing Southeast Asia at its apex and again, Thule and Pre-Inca as the base. This telescoping effect of Mongolia/Thule-Pre-Inca and then Southeast Asia/Thule-Pre-Inca suggests an approximate age equivalence of Thule and Pre-Inca samples, and is also compatible with the data of Cavalli-Sforza et al. (1988) that showed genetic separation between northern and southern Mongoloids. Although intermediate between Southeast Asians and Native Americans, Mongolia is oddly offset as if a hidden attractor, or

¹There is an autosomal dominant dentin defect [dentin dysplasia type I (Shields et al., 1973)] and several genetic syndromes with abbreviated tooth roots, e.g., postaxial polydactyly-dental-vertebral syndrome. E.D.S. has identified (unpublished observation) a Greek child with ubiquitous abbreviated roots and maxillary anterior dens-in-dente anomalies.

TABLE 2. A summary of some important variables used for the univariate analysis of the total dental phenotype

Ethnic group	N Obs	Variable	Mean	Standard deviation	Coefficient of variation
Southern Chinese	330	Tooth height	21.618	2.948	13.636
		Elongation	0.313	0.120	38.493
		Distal enamel	0.662	0.189	28.531
		Relative pulp area	0.099	0.024	24.666
		Crown/root ratio	0.915	0.205	22.427
Vietnamese	342	Tooth height	23.383	3.059	13.083
		Elongation	0.261	0.107	40.883
		Distal enamel	0.621	0.220	35.450
		Relative pulp area	0.113	0.027	23.526
		Crown/root ratio	0.931	0.218	23.447
Mongolians	800	Tooth height	22.154	3.064	13.832
		Elongation	0.283	0.115	40.620
		Distal enamel	0.663	0.198	29.828
		Relative pulp area	0.111	0.030	27.085
		Crown/root ratio	0.909	0.245	26.957
Western Inuit	369	Tooth height	22.269	3.125	14.033
		Elongation	0.278	0.112	40.475
		Distal enamel	0.705	0.225	31.888
		Relative pulp area	0.123	0.035	28.699
		Crown/root ratio	0.847	0.201	23.716
Thule	548	Tooth height	20.409	3.552	17.403
		Elongation	0.364	0.153	41.981
		Distal enamel	0.683	0.206	30.204
		Relative pulp area	0.126	0.035	28.085
		Crown/root ratio	0.913	0.223	24.473
Dorset	142	Tooth height	20.799	3.546	17.048
		Elongation	0.357	0.155	43.529
		Distal enamel	0.706	0.209	29.549
		Relative pulp area	0.122	0.042	34.282
		Crown/root ratio	0.867	0.184	21.231
Pre-Inca	264	Tooth height	21.761	3.513	16.143
		Elongation	0.333	0.142	42.615
		Distal enamel	0.827	0.249	30.150
		Relative pulp area	0.121	0.036	29.734
		Crown/root ratio	0.870	0.208	23.859

unmeasured related population facing away from Mongolia is pulling on it (Shields, 1996). The independence or distinctiveness of the Southampton Island sample from the Thule and its pivotal position as the epicenter of the major cluster suggests that this sample is composed of Paleoeskimo (Dorset), and is labeled as "Dorset" for the rest of this study.

Southampton Island lies in the northern part of Hudson Bay bordering the Foxe Basin. Although it is positioned relatively close to the Keewatin mainland, the treacherous currents of Roes Welcome and the movement of coastal ice (Leden, 1990; Merbs, 1983) act as natural barriers to the passage of people. A Dorset community existed on this outpost (McGhee, 1996). A few dozen Sadlermiut people persisted on Southampton Island until 1902 when all but five died of an epidemic introduced by European whalers (Leden, 1990). Archaeological (Clark, 1980; Collins 1958; Merbs, 1983; Taylor,

1960), ethnographic (Mathiassen, 1927a; Merbs, 1983), and linguistic (Mathiassen, 1927b; Taylor, 1962) data, Neoinuit oral tradition (Pelly, 1987; Leden, 1990), and European whaler accounts (Hrdlička, 1910; Pelly, 1987; Leden, 1990) all strongly suggest that the Southampton Island population spectrum at Sadlermiut was a far outlier among the very uniform Central Arctic Inuit people. Hrdlička (1910) believed that the closest relatives of the Southampton Sadlermiut were the Western Inuit and not their neighbors in Central Canada. Collins (1958) and Clark (1980) summarized the data by suggesting that the Sadlermiut may have been related to the old Dorset people on the island, with Thule influence. In disagreement, Utermohle's (1984/1993) assessment of skeletal material failed to show biological deviance of the Sadlermiut from Thule/Inuit.

There are peripheral data suggesting that Dorset groups persevered many hundred

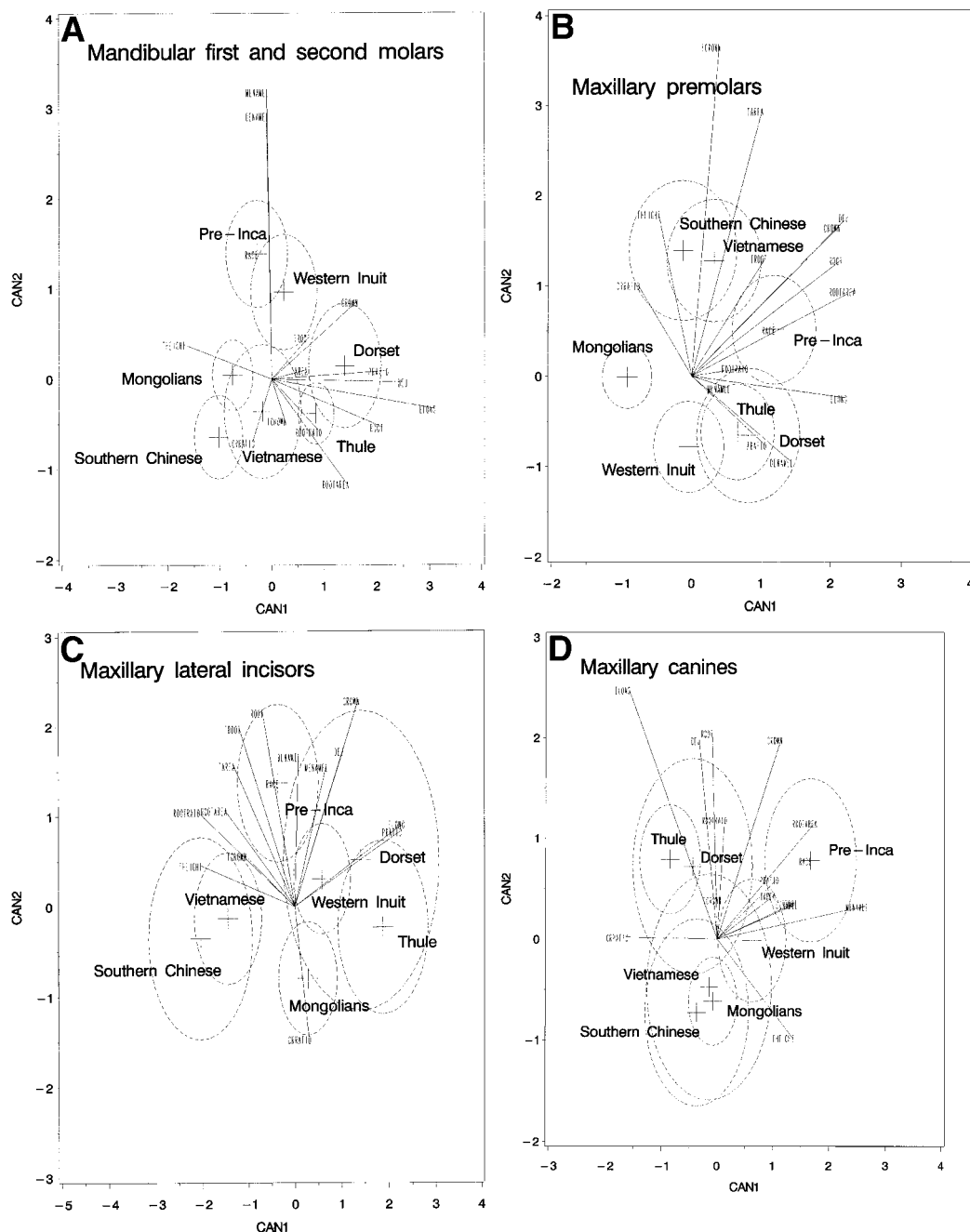


Fig. 4. Four representative tooth elements were chosen to demonstrate the 2-D separation among the ethnic stocks and the strength of each the variable in the separation: **A)** mandibular first and second molars, **B)** maxillary premolars, **C)** maxillary lateral incisors, and **D)** maxillary canines.

years (Taçon, 1983) after their presumed extinction ~1100 AD. Plumet (1979) and Thomson (1982) presented data supporting a late persistence of relic Dorset enclaves to perhaps the 1550s in an area of Ungava Bay

in northern Quebec and Labrador. Southampton Island lies on a straight line from this area along the Hudson Strait. More isolated sites in eastern Greenland also had signs of Dorset persistence (Meldgaard, 1967;

TABLE 3. Pairwise Mahalanobis' D^2 distances among the Southeast Asian, east Central Asian, and Native American samples

Population	S. China	Vietnam	Mongolia	W. Inuit	Dorset	Thule	Pre-Inca
S. China	—						
Vietnam	0.776	—					
Mongolia	1.151	1.353	—				
W. Inuit	1.940	1.652	0.447	—			
Dorset	1.362	1.804	0.698	0.671	—		
Thule	2.018	2.221	1.493	1.387	0.752	—	
Pre-Inca	2.122	1.977	1.316	0.550	0.737	1.652	—

Jordan, 1984) and possible admixture with Thule (Bandi and Meldgaard, 1952).

The data presented here suggest that the insular Sadlermiut were mainly genetically Dorset who because of their isolation had persisted within the relative cultural and genetic homogeneity of the widespread and diffuse Canadian Arctic and Greenland Thule culture Inuit. Inadvertent cultural factors likely helped mitigate the effects of inbreeding through interaction with other remnant Dorset within their isolated cultural archipelago (perhaps with communities in Ungava and even Greenland, or with a yet to be identified communities). The isolated position of the Thule at the periphery of the major subcluster of Mongolia-Western Inuit-Dorset-Pre-Inca and the small Thule population size are compatible with random genetic drift as a major factor in Thule dental change. The population structure of the Dorset predisposed them to equal, if not greater opportunity for genetic drift-driven effects. It thus can be argued that the small Southampton Island sample either did not capture the full extend of Dorset variation and thus their central position within the major subcluster is anomalous, or the disparity between the Southampton Island sample and Thule was the result of genetic drift within Thule. Unknown population dynamic factors and the indeterminacy of a Native American root, documented as a conspicuous space near the origin of Figure 2, makes interpretation challenging. Finding skeletal material from an extinct east Asian antecedent population and teeth from extinct Dorset would allow tests of these hypotheses.

A lack of a major reversal of the Dorset/Thule trajectory back toward Southeast Asia, implies that the genetic influence from the west when the Dorset culture first appeared in the archaeological record was much less

significant than its cultural impact (West, 1996). With recognition of the potential for overinterpretation, the Western Inuit sample had the shortest distance to their Mongolian "sibling" population and thus may have received some recurrent gene flow from east Central Asia into America toward the end of the migratory wave. The proximity of the Western Inuit and Pre-Inca suggests admixture between Western Inuit and Amerindians. The addition of further populations derived from the Beringian founders, i.e., more Amerind populations, Na-Déné, and Aleuts, should help clarify the biologic meaning of the observed distances. In agreement with Szathmáry (Szathmáry and Ossenberg, 1978; Szathmáry 1979, 1981, 1993, 1996), the data presented here suggest that the Thule/Inuit-Western Inuit lineage developed autochthonously within Beringia from Paleoindian founders, and from the same general Beringian population source as the Dorset. Perhaps some of the Beringia migrants were not itinerant, but persisted on the coast and were not forced south by the severe conditions of the Younger Dryas, the last major cold oscillation. These people became the Paleoindian.

North America had at the time of the Paleoindian colonization a different environment from today. It is easy for the modern perspective to intrude into the reality that our distant relatives survived. The unique nature of the American environment encountered by these first immigrants, an environment with no known history of human environmental modification, a vastness of great scale, and the likelihood that pioneers would encounter new pathogens and dietary substances (Shields, unpublished) would predispose to genetic drift or selection. Differentiation within Beringia could have been forced by climatic diversity of Beringia (e.g., cold

versus moderate climate, coastal versus inland adaptations) or severe habitat stress that forced people to emigrate (Amsden, 1979). The history of Native Americans is nonlinear. It can be postulated on cultural similarities of Alaskan and Siberian archeologic sites that Dyuktai people were the northeast Asian founder group that expanded from east Central Asia [as suggested from Nei's hypothesis (1995)] to Beringia (Mochanov and Fedoseeva, 1996), i.e., the Selemdya-Dyuktai-Denali continuum (West, 1996). If correct, a significant time gap exists in archaeological sites from Asian Upper Paleolithic Dyuktai sites (Mochanov and Fedoseeva, 1996) to the much more recent Denali sites in Alaska (~12,000 BP). One can only wonder what coastal Beringia information lies under the Bering Strait. Interestingly, the Denali complex represents the precursors of the Dorset, thus adding further support to our result of the ancient nature of the potential Dorset sample described here. After the end of the Pleistocene, cultural exchange, or reflux back to Asia (Karafet et al., 1997), occurred between America and northeast Asia, i.e., Ekven and Uelen associations with Old Bering Sea culture (Yamaura, 1979). Indeed, it is unlikely that the people in Beringia cut off contacts with their relatives, thus helping to account for a migratory "wave." It is also probable that their pivotal bridge-holding position allowed Beringians to block the immigration into America of explorers from alien cultures.

The vagaries of the harsh and dynamic Arctic environment and small population sizes during most of Native American history (Ubelaker, 1988) predispose to genetic bottlenecks and resulting genetic drift (Livshits and Nei, 1990), or extinction (Lande, 1994). If a sample of Native American founders were in fact able to persist on the Beringia coast, the induced severe environmental stress of the Younger Dryas cold spell [~13,000 – ~11,500 BP (Edwards et al., 1993)] could have caused a genetic bottleneck in this group. Such a bottleneck may be indicated by the loss of mtDNA haplogroups among the Inuit and Athapaskans as compared to most Amerinds (Shields et al., 1993). Nonetheless, the nonrandom distribution of genes in the sample of Paleoindians that remained in Beringia may be a suffi-

cient explanation for the missing mtDNA haplogroups, because the global dental phenotype showed no sign that the Younger Dryas caused a bottleneck. The Paleoindian were seemingly not as limited by severe and harsh climate as they were by the availability of foodstuff (Jacobs, 1979; Fagan, 1995). A genetic sign of a bottleneck in at least one Western Inuit group has been documented (Speiser et al., 1992).

The recent nature of the Thule radiation, a genetic bottleneck (Forster et al., 1996) in Thule founders, or both, are compatible with an observed lack of Inuit genetic and linguistic diversity (Dumond, 1987). Regardless, the low level of genetic differentiation found among modern-day but insular Inuit could also be a consequence of the Thule/Inuit preference to seek distant relations for mates, a result of their nomadic life style (Kolman et al., 1996), trade and trade fairs (Hickey, 1979), and other cultural practices that could have affected mating behaviors. Compatible with this notion is the finding of a small inbreeding coefficient in a very small Eastern Inuit community (Edwards, 1992), conditions under which a larger value would be expected, and as suggested here, the persistence of a remnant Dorset community.

The emergence of the Thule culture was a recent development (roughly equivalent to the beginning of the Christian era), with its epicenter in northern Alaska. The Thule rapidly extended throughout the territory of the Dorset, all the way to Greenland. In true Darwinian fashion, the Thule likely caused the rapid demise of the Dorset either through the introduction of disease (Rowley, 1985; McGhee, 1994) for which the Dorset were immunologically naive, warfare, or a combination of both. The data presented here show little, if any, sign of Dorset/Thule admixture.

Figures 2 and 3 document East Asian and Native American dental microevolution and descent. There were no overall trends among the populations, but there were disparate changes affecting multiple genetic determinants in a seemingly random or chaotic fashion, as expected for genetic drift. Among the groups, Thule and Dorset had short but robust teeth, with large relative pulp areas and thinner enamel. For a population that appeared to rely so heavily on their teeth for

survival, undoubtedly the global dental phenotype was not a factor in their fitness. If directional selection were at work, we would expect that Thule/Dorset would tend to have large teeth with long, robust roots, thick enamel, and minimal pulp space. Generally, the observed variation was also global; e.g., genes inducing thinner enamel per se, and not tooth element-specific differences. The drift-induced genotype of the Inuit could have put this population on the path to tooth root elimination.

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